

# SEQUENCE LISTING

<110> Taylor, Alexander H

<120> Monoclonal Antibodies with Reduced Immunogenicity

<130> P50770

&lt;150&gt; 60/083.367

<151> 1998-04-28

&lt;160&gt; 97

<170> FastSEQ for Windows Version 3.0

 $\langle 210 \rangle$  1

&lt;211&gt; 429

&lt;212&gt; DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1) . . . (429)

 $\langle 400 \rangle$  1

atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

1                      5                      10                      15

gtc ctg tcc cag gtg cag ttg cag gag tcg ggc cca gga ctg gtg aag 96

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys

20                      25                      30

cct tca cag acc ttg tcc ctg acc tgc gct gtg tct ggt ggc tcc atc 144

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile

35	40	45	
act agt gct tac tac tat tgg agc tgg atc cgc cag tca cca ggg aag			192
Thr Ser Ala Tyr Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys			
50	55	60	
gga ctg gag tgg att ggg agt atc tat tat agt ggg acc att ttc tcc			240
Gly Leu Glu Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Thr Ile Phe Ser			
65	70	75	80
aac cca tcc ctc aag agt cga gtc gcc atg tca gta ggc acg tcc aag			288
Asn Pro Ser Leu Lys Ser Arg Val Ala Met Ser Val Gly Thr Ser Lys			
85	90	95	
acc cag ttc tcc ctg agc ttg agt tct gtg acc gcc gcg gac acg gcc			336
Thr Gln Phe Ser Leu Ser Leu Ser Ser Val Thr Ala Ala Asp Thr Ala			
100	105	110	
gtg tac tac tgt gcg aga ggt ctg ctc ctc acc att gga ctg acc aac			384
Val Tyr Tyr Cys Ala Arg Gly Leu Leu Leu Thr Ile Gly Leu Thr Asn			
115	120	125	
tac tac ttt gac tac tgg ggc ccg gga acc ctg gtc acc gtc ttc			429
Tyr Tyr Phe Asp Tyr Trp Gly Pro Gly Thr Leu Val Thr Val Phe			
130	135	140	

&lt;210&gt; 2

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(414)

&lt;400&gt; 2

atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg	48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
1 5 10 15	
gtc ctg tcc cag gtg cag cta cag gag tgg ggc cca gga cta gtg aag	96
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	
20 25 30	
ccg tca cag acc ctg tcc ctc acc tgc ggt gtc tct ggt gcc tcc atc	144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Gly Val Ser Gly Ala Ser Ile	
35 40 45	
aat agt ggt gtt cat tac tgg gcc tgg ata cgc cag cct gca gga aag	192
Asn Ser Gly Val His Tyr Trp Ala Trp Ile Arg Gln Pro Ala Gly Lys	
50 55 60	
gga ctg gag tgg att ggc aat atc tat cat agt ggg agc gcc tac tac	240
Gly Leu Glu Trp Ile Gly Asn Ile Tyr His Ser Gly Ser Ala Tyr Tyr	
65 70 75 80	
act cca tcc ctc gag agt cga gtc tcc atg tca ata gag acg tcc aag	288
Thr Pro Ser Leu Glu Ser Arg Val Ser Met Ser Ile Glu Thr Ser Lys	
85 90 95	
agc cag ttc ttc cta aac tta aat tct ctg acc gcc gcg gac acg gct	336
Ser Gln Phe Phe Leu Asn Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala	
100 105 110	
atc tat tat tgt gcg aga cga cat act tcg tca gac tac ttt gac ttt	384
Ile Tyr Tyr Cys Ala Arg Arg His Thr Ser Ser Asp Tyr Phe Asp Phe	
115 120 125	
tgg ggc cgc gga atc ctg gtc atc gtc tcc	414
Trp Gly Arg Gly Ile Leu Val Ile Val Ser	
130 135	



tac tac tgt gcg agc cga aat cac ttt gtt ttc ggg gaa gtt att act 384  
 Tyr Tyr Cys Ala Ser Arg Asn His Phe Val Phe Gly Glu Val Ile Thr  
 115 120 125

act ttg acg gct ggg gcc agg gaa acc ctg ggt cac cgt ctc c 427  
 Thr Leu Thr Ala Gly Ala Arg Glu Thr Leu Gly His Arg Leu  
 130 135 140

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 <213> Pan troglodytes

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 <222> (1)...(402)

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 Leu Gly Leu Arg Trp Val Phe Leu Val Ala Phe Leu Glu Gly Val Gln  
 1 5 10 15

tgt gag gta cag ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg 96  
 Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly  
 20 25 30

ggg tcc ttg aca ctc tcc tgt gca gcc tct gga ttc acc ttc agt agg 144  
 Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg  
 35 40 45

agt ggc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg ggg tgg 192  
 Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gly Trp  
 50 55 60

ctt gca tac att gat tat ggc agt att ttc ata tac tac tcg gac tca 240

Leu Ala Tyr Ile Asp Tyr Gly Ser Ile Phe Ile Tyr Tyr Ser Asp Ser  
 65 70 75 80  
 gtg aag ggc cgc ttc acc atc tcc aga gac aac gcc aag aat tca ctc 288  
 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu  
 85 90 95  
 tat ctg caa atg aac agc ctg aga gcc gac gac acg gct ttt tat tac 336  
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Phe Tyr Tyr  
 100 105 110  
 tgt acg acc cat aat tgg ggg gag tta act gac tac tgg ggc cag gga 384  
 Cys Thr Thr His Asn Trp Gly Glu Leu Thr Asp Tyr Trp Gly Gln Gly  
 115 120 125  
 acc ctg gtc acc gtc tcc 402  
 Thr Leu Val Thr Val Ser  
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 <221> CDS  
 <222> (1)...(408)  
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 Met Glu Leu Gly Leu Arg Trp Val Phe Leu Val Ala Phe Leu Glu Gly  
 1 5 10 15  
 gtc cag tgt gag gta cag ctg gtg gag tct ggg gga ggc ttg gta cag 96  
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
 20 25 30

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cct ggg ggg tcc ttg aca ctc tcc tgt gca gcc tct gga ttc acc ttc      144
Pro Gly Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
      35                      40                      45

agt agg agt ggc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg      192
Ser Arg Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
      50                      55                      60

gag tgg ctt gca tac att gat tat ggc agt att ttc ata tac tac tcg      240
Glu Trp Leu Ala Tyr Ile Asp Tyr Gly Ser Ile Phe Ile Tyr Tyr Ser
      65                      70                      75                      80

gac tca gtg aag ggc cgc ttc acc atc tcc aga gac aac gcc aag aat      288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
      85                      90                      95

tca ctc tat ctg caa atg aac agc ctg aga gcc gac gac acg gct ttt      336
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Phe
      100                      105                      110

tat tac tgt acg acc cat aat tgg ggg gag tta act gac tac tgg ggc      384
Tyr Tyr Cys Thr Thr His Asn Trp Gly Glu Leu Thr Asp Tyr Trp Gly
      115                      120                      125

cag gga acc ctg gtc acc gtc tcc      408
Gln Gly Thr Leu Val Thr Val Ser
      130                      135

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&lt;210&gt; 6

&lt;211&gt; 421

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(421)

&lt;400&gt; 6

atg atg ggg tca acc gcc atc ctc gcc ctc ctc ctg gct gtt ctc caa	48
Met Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln	
1 5 10 15	
gga gtc tgt gca gag gtg cag ctg gtg cag tct gga gca gag gtg aaa	96
Gly Val Cys Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys	
20 25 30	
aag ccc ggg gag tct ctg aag atc tcc tgt aag ggc tct gga tac agt	144
Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser	
35 40 45	
ttt acc aac tac tgg atg ggc tgg gtg tgc cag atg ccc ggg aaa ggc	192
Phe Thr Asn Tyr Trp Met Gly Trp Val Cys Gln Met Pro Gly Lys Gly	
50 55 60	
ccg gag tgc atg ggg atc atc tat cct gat gac tct gat acc aga tac	240
Pro Glu Cys Met Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr	
65 70 75 80	
agc ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc	288
Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile	
85 90 95	
agc acc gcc tac cta caa tgg agc aac ctg aag gcc tgc gac acc gcc	336
Ser Thr Ala Tyr Leu Gln Trp Ser Asn Leu Lys Ala Ser Asp Thr Ala	
100 105 110	
ata tat tac tgt gcg aga tgt tat ggt tgg act act tgc gaa gct ttt	384
Ile Tyr Tyr Cys Ala Arg Cys Tyr Gly Trp Thr Thr Cys Glu Ala Phe	
115 120 125	
gat atc tgg ggc caa ggg aca atg gtc acc gtc tct t	421
Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser	



140

<213> Pan troglodytes

 $\langle 222 \rangle \quad (1) \dots (417)$ 

ttg tgg ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc 48  
 Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser  
 1 5 10 15

cag ctg cag ctg cag gag tgc gcc cca gga ctg gtg aag cct tca cag 96  
Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
20 25 30

acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agc agt ggt 144  
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly  
35 40 45

agt tac tac tgg agt tgg atc cgg cag ccc gcc ggg aag cga ctg gag 192  
 Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Arg Leu Glu  
 50 55 60

tgg att ggg tat att tat tat agt ggg agt acc tac tac aac cca tcc 240  
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser  
65 70 75 80

ctc aag agt cga gtc acc ata tca gta gac acg tcc aag aac cag ttc 288  
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe  
85 90 95

tcc ctg aag ctg agc tct gtg acc gcc gca gac acg gcc gtc tat tac 336  
 Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
 100 105 110

tgt gcg aga tct ccc caa aac gta tta caa tct ttg gac tgc ttc gac 384  
 Cys Ala Arg Ser Pro Gln Asn Val Leu Gln Ser Leu Asp Cys Phe Asp  
 115 120 125

ccc tgg ggc cag gga acc ctg gtc acc gtc tcc 417  
 Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
 130 135

<210> 8  
 <211> 369  
 <212> DNA  
 <213> Pan troglodytes

<220>  
 <221> CDS  
 <222> (1)...(369)

<400> 8  
 gtc cag tcc cag gtc cag ctg gtg cag tcc ggg gct gag gtg aag aag 48  
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 1 5 10 15

cct ggg tcc tca gtg aag gtc tcc tgc aag gtt tcc gga ggc acc ttc 96  
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Val Ser Gly Gly Thr Phe  
 20 25 30

agc acc tat ggt ttc agc tgg gtg cgg cag gcc cct gga caa ggg ctt 144  
 Ser Thr Tyr Gly Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 35 40 45

gag tgg atg gga atg atc atc cct atc gtt ggc aca gta aag tac gca 192  
 Glu Trp Met Gly Met Ile Ile Pro Ile Val Gly Thr Val Lys Tyr Ala

50

55

60

cag agg ttc cag ggc aga gtc tca att aat gcg gac aca tcc acg aat 240  
 Gln Arg Phe Gln Gly Arg Val Ser Ile Asn Ala Asp Thr Ser Thr Asn  
 65 70 75 80

ata gcc tac atg gag ctg acc agc ctg aga tct gag gac acg gcc gtc 288  
 Ile Ala Tyr Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val  
 85 90 95

tat tac tgt gcg aca gat ctg acg gtg act act aat gat gca ttt gat 336  
 Tyr Tyr Cys Ala Thr Asp Leu Thr Val Thr Thr Asn Asp Ala Phe Asp  
 100 105 110

atc tgg ggc caa ggg aca atg gtc acc gtc tct 369  
 Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser  
 115 120

&lt;210&gt; 9

&lt;211&gt; 423

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(423)

&lt;400&gt; 9

atg gag ttt ggg ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt 48  
 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly  
 1 5 10 15

gtc cag tgt gag gtg cag ctg gtg gag tct ggg gaa ggc ttg gta aag 96  
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Glu Gly Leu Val Lys  
 20 25 30

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<210> 10
<211> 97
<212> PRT
<213> Pan troglodytes
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38

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (52)...(67)

&lt;223&gt; CDRII

&lt;400&gt; 10

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gln
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Ser	Gly	Gly	Ser	Ile	Thr	Ser	Ala
			20					25					30		
Tyr	Tyr	Tyr	Trp	Ser	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	Glu
		35				40						45			
Trp	Ile	Gly	Ser	Ile	Tyr	Tyr	Ser	Gly	Thr	Ile	Phe	Ser	Asn	Pro	Ser
		50				55					60				
Leu	Lys	Ser	Arg	Val	Ala	Met	Ser	Val	Gly	Thr	Ser	Lys	Thr	Gln	Phe
65				70					75					80	
Ser	Leu	Ser	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr
				85					90					95	

Cys

&lt;210&gt; 11

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(37)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (52)...(67)

&lt;223&gt; CDRII

&lt;400&gt; 11

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Gly Val Ser Gly Ala Ser Ile Asn Ser Gly  
 20 25 30  
 Val His Tyr Trp Ala Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu  
 35 40 45  
 Trp Ile Gly Asn Ile Tyr His Ser Gly Ser Ala Tyr Tyr Thr Pro Ser  
 50 55 60  
 Leu Glu Ser Arg Val Ser Met Ser Ile Glu Thr Ser Lys Ser Gln Phe  
 65 70 75 80  
 Phe Leu Asn Leu Asn Ser Leu Thr Ala Asp Thr Ala Ile Tyr Tyr Cys  
 85 90 95

<210> 12  
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 <212> PRT  
 <213> Pan troglodytes

<220>  
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 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 12

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15  
 Ser Leu Lys Ile Ser Cys Lys Val Ser Gly Asn Glu Phe Thr Asn Tyr  
 20 25 30  
 Trp Ile Ala Trp Val Arg Gln Met Ser Gly Lys Gly Leu Glu Trp Met  
 35 40 45  
 Gly Ser Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Asn Pro Ser Phe  
 50 55 60  
 Gln Gly Gln Val Thr Phe Ser Ala Asp Lys Ser Ile Thr Thr Ala Tyr

65		70		75		80									
Leu	Gln	Trp	Ser	Ser	Leu	Glu	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
				85					90					95	

<210> 13  
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 <213> Pan troglodytes

<220>  
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 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 13

Asp	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1			5						10					15	
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Val	Ser	Gly	Asn	Glu	Phe	Thr	Asn	Tyr
			20						25					30	
Trp	Ile	Ala	Trp	Val	Arg	Gln	Met	Ser	Gly	Lys	Gly	Leu	Glu	Trp	Met
			35				40					45			
Gly	Ser	Ile	Tyr	Pro	Gly	Asp	Ser	Asp	Thr	Arg	Tyr	Asn	Pro	Ser	Phe
			50				55				60				
Gln	Gly	Gln	Val	Thr	Phe	Ser	Ala	Asp	Lys	Ser	Ile	Thr	Thr	Ala	Tyr
			65				70				75			80	
Leu	Gln	Trp	Ser	Ser	Leu	Glu	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
				85					90					95	

<210> 14  
 <211> 96  
 <212> PRT  
 <213> Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 14

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Thr	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Ser
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Gly	Trp	Leu
		35					40					45			
Ala	Tyr	Ile	Asp	Tyr	Gly	Ser	Ile	Phe	Ile	Tyr	Tyr	Ser	Asp	Ser	Val
		50				55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
65					70					75				80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Phe	Tyr	Tyr	Cys
				85					90					95	

&lt;210&gt; 15

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII



&lt;400&gt; 15

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15  
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr  
 20 25 30  
 Trp Met Gly Trp Val Cys Gln Met Pro Gly Lys Gly Pro Glu Cys Met  
 35 40 45  
 Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60  
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80  
 Leu Gln Trp Ser Asn Leu Lys Ala Ser Asp Thr Ala Ile Tyr Tyr Cys  
 85 90 95

&lt;210&gt; 16

&lt;211&gt; 97

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(37)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (52)...(67)

&lt;223&gt; CDRII

&lt;400&gt; 16

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly  
 20 25 30  
 Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Arg Leu Glu  
 35 40 45  
 Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser  
 50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe  
 65 70 75 80  
 Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
 85 90 95  
 Cys

<210> 17  
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<220>  
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 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

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 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Val Ser Gly Gly Thr Phe Ser Thr Tyr  
 20 25 30  
 Gly Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
 35 40 45  
 Gly Met Ile Ile Pro Ile Val Gly Thr Val Lys Tyr Ala Gln Arg Phe  
 50 55 60  
 Gln Gly Arg Val Ser Ile Asn Ala Asp Thr Ser Thr Asn Ile Ala Tyr  
 65 70 75 80  
 Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

<210> 18  
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<212> PRT  
 <213> Pan troglodytes

<220>  
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 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 18  
 Glu Val Gln Leu Val Glu Ser Gly Glu Gly Leu Val Lys Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe  
 20 25 30  
 Leu Met Phe Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Thr Ile Asp Val Ser Gly Gly Asn Met Trp Tyr Arg Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Met Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Thr Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

<210> 19  
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 <212> DNA  
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<220>  
 <221> CDS  
 <222> (1)...(381)

<400> 19  
 atg agg gtc cct gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc tca 48

46

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(384)

&lt;400&gt; 20

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg	48
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp	
1 5 10 15	
ctc cca ggt acc aga tgt gac atc cag atg acc cag tct cca tcc tcc	96
Leu Pro Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
20 25 30	
ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gcc agt	144
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser	
35 40 45	
cag ggc att agc aat tat tta gcc tgg tat cag cag aaa cca ggg aaa	192
Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys	
50 55 60	
gcc cct aag ctc ctc atc tat tat gca tcc aga ttg gaa agt ggg gtc	240
Ala Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Arg Leu Glu Ser Gly Val	
65 70 75 80	
cca tca agg ttc agc ggc agt gga tct ggg acg gat tac act ctc acc	288
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr	
85 90 95	
atc agc agc ctg cag cct gaa gat ttt gca act tat tac tgt caa cag	336
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln	
100 105 110	
tat aac agt aac ccc ttt tcg gtg gag gga cca agg tgg aga tca aac	384
Tyr Asn Ser Asn Pro Phe Ser Val Glu Gly Pro Arg Trp Arg Ser Asn	
115 120 125	

<210> 21  
 <211> 384  
 <212> DNA  
 <213> Pan troglodytes

<220>  
 <221> CDS  
 <222> (1)...(384)

<400> 21

atg tcg cca tca caa ctc att ggg ttt ctg ctg ctc tgg gtt cca gcc 48  
 Met Ser Pro Ser Gln Leu Ile Gly Phe Leu Leu Leu Trp Val Pro Ala  
 1 5 10 15

tcc agg ggt gaa att gtg ctg act cag tct cca gac ttt cag tct gtg 96  
 Ser Arg Gly Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val  
 20 25 30

cct cca aag gag aaa gtc acc atc acc tgc cgg gcc agt cag agc att 144  
 Pro Pro Lys Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile  
 35 40 45

ggc agt agc tta cac tgg tac cag cag aaa cca ggt cag tct cca aag 192  
 Gly Ser Ser Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
 50 55 60

ctc ctc atc aag tat gct tcc cag tcc atc tca ggg gtc ccc tcg agg 240  
 Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Val Pro Ser Arg  
 65 70 75 80

ttc agt ggc agt gga tct ggg aca gat ttc acc ctc acc atc aat agc 288  
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser  
 85 90 95

ctg gaa gct gaa gat gct gca acg tat tac tgt cag caa agt agt aat 336  
 Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Asn

100

105

110

tta cct cat acg ctc act ttc ggt gga ggg acc aag gtg gag atc aaa 384  
 Leu Pro His Thr Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 115 120 125

&lt;210&gt; 22

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(372)

&lt;400&gt; 22

gtc cct gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc tca ggt gcc 48  
 Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu Ser Gly Ala  
 1 5 10 15

aga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct 96  
 Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser  
 20 25 30

gta gga gac aga gtc acc atc act tgc cag gca agt cag agc att agc 144  
 Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser  
 35 40 45

aac tat ttg agt tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc 192  
 Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu  
 50 55 60

ctg atc tat gat gca tcc act ttg caa agt ggg gtc cca tca agg ttc 240  
 Leu Ile Tyr Asp Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe  
 65 70 75 80

agt ggc agt gga tct ggg aca gat ttc act ctc acc atc agc agt ctg 288  
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu  
 85 90 95

caa cct gaa gat ttt gca aca tat tac tgt cag cgt ggt tac ggt aca 336  
 Gln Pro Glu Asp Phe Ala Thr Tyr Cys Gln Arg Gly Tyr Gly Thr  
 100 105 110

ctc act ttc ggt gga ggg acc aag gtg gag atc aaa 372  
 Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 115 120

<210> 23  
 <211> 384  
 <212> DNA  
 <213> Pan troglodytes

<220>  
 <221> CDS  
 <222> (1)...(384)

<400> 23  
 atg gaa gcc cca gcg cag ctt ctc ttc ctc ctg cta ctc tgg ctc cca 48  
 Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro  
 1 5 10 15

gat acc acc gga gaa ata gtg ttg acg cag tct cca gcc acc ctg tct 96  
 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser  
 20 25 30

ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt 144  
 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser  
 35 40 45

gtt agc agg tac tta gcc tgg tac cag cag aaa cct gcc cag gct ccc 192  
 Val Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro



50	55	60	
agg ctc ctc atc tat ggt gca tcc aac agg gcc act ggc atc cca gcc			240
Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala			
65	70	75	80
agg ttc agt ggc agt ggg tct agg aca gac ttc act ctc acc atc agc			288
Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Ser			
85	90	95	
agc gtg gag cct gaa gat ttt gca gtt tat tac tgt cag cag tat aat			336
Ser Val Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn			
100	105	110	
aac cag cct ctg atc gcc ttc ggc caa ggg aca cga ctg gag att aaa			384
Asn Gln Pro Leu Ile Ala Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys			
115	120	125	
<210> 24			
<211> 387			
<212> DNA			
<213> Pan troglodytes			
<220>			
<221> CDS			
<222> (1)...(387)			
<400> 24			
atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg			48
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp			
1	5	10	15
ttc cca ggt gcc aaa tgt gac atc cag atg acc cag tct cct tcc acc			96
Phe Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Thr			
20	25	30	



53

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(372)

&lt;400&gt; 26

tct act cag ctc ctg ggg ctc ctg ctg ctc tgg ctc cca ggt gcc aaa 48  
 Ser Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro Gly Ala Lys

1 5 10 15

tgt gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct gta 96  
 Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val

20 25 30

gga gac aga gtc acc atc act tgc cgg gcc agt cag ggt att agt agc 144  
 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser

35 40 45

tgg tta gcc tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg 192  
 Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu

50 55 60

atc tat aag gca tct agt tta gaa agt ggg gtc cca tca agg ttc agc 240  
 Ile Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser

65 70 75 80

ggc agt gga tct ggg aca gaa ttc act ctc acc atc agc agc ctg cag 288  
 Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln

85 90 95

cct gat gat ttt gca act tat tac tgc caa cag tat agt agt tac cct 336  
 Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser Tyr Pro

100 105 110

cga acg ttc ggc caa ggg acc aag ctg gaa atc aaa 372  
 Arg Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

115 120

<210> 27  
 <211> 387  
 <212> DNA  
 <213> Pan troglodytes

<220>  
 <221> CDS  
 <222> (1)...(387)

<400> 27

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg	48
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp	
1 5 10 15	
ctc tca ggt acc aga tgt gac atc cag atg acc cag tct cca tcc tcc	96
Leu Ser Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
20 25 30	
ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt	144
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser	
35 40 45	
cag agc att agc aac tat ttg agt tgg tat cag cag aaa cca ggg aaa	192
Gln Ser Ile Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys	
50 55 60	
gcc cct aag ctc ctg atc tat tat gca tcc act ttg caa agt ggg gtc	240
Ala Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Gln Ser Gly Val	
65 70 75 80	
cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act ctc acc	288
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
85 90 95	
atc agc agt ctg caa cct gaa gat ttt gca act tat tac tgt cag cat	336



<210> 29  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 29

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Asn	Tyr
			20					25						30	
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
			35					40					45		
Tyr	Tyr	Ala	Ser	Arg	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
			50				55					60			
Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
			65				70				75			80	
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys								
							85								

<210> 30  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

&lt;223&gt; CDR11

<400> 30

[illegible]

&lt;210&gt; 31

&lt;211&gt; 88

&lt;212&gt; PRT

<213> Pan troglodytes

<220>

&lt;221&gt; DOMAIN

 $\langle 222 \rangle \quad (24) \dots (34)$ 

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

<222> (50) . . . (66)

&lt;223&gt; CDR11

&lt;400&gt; 31

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Asn Tyr



20 25 30  
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Asp Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys  
 85

<210> 32  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 32

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr  
 20 25 30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
 35 40 45  
 Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Glu Pro  
 65 70 75 80  
 Glu Asp Phe Ala Val Tyr Tyr Cys  
 85

<210> 33  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 33

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly
 1             5             10             15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Tyr Asn Tyr
 20             25             30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro Gly Leu Leu Ile
 35             40             45
Phe Gly Ala Arg Asn Leu Glu Thr Gly Val Pro Ser Thr Phe Ser Gly
 50             55             60
Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65             70             75             80
Gly Asp Phe Ala Thr Tyr Tyr Cys
 85

```

<210> 34  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 34

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1             5             10             15
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Leu Asp Ile Ser Thr Trp
             20             25             30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile
             35             40             45
Tyr Ala Ala Ser Thr Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly
             50             55             60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
             65             70             75             80
Glu Asp Ser Ala Thr Tyr Tyr Cys
             85

```

&lt;210&gt; 35

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 35

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1             5             10             15

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
      20                      25                      30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
      35                      40                      45
Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
      50                      55                      60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
      65                      70                      75                      80
Asp Asp Phe Ala Thr Tyr Tyr Cys
      85

```

```

<210> 36
<211> 88
<212> PRT
<213> Pan troglodytes

```

```

<220>
<221> DOMAIN
<222> (24)...(34)
<223> CDRI

```

```

<221> DOMAIN
<222> (50)...(66)
<223> CDRII

```

```

<400> 36

```

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
      1                      5                      10                      15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
      20                      25                      30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
      35                      40                      45
Tyr Tyr Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
      50                      55                      60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
      65                      70                      75                      80
Glu Asp Phe Ala Thr Tyr Tyr Cys

```

85

<210> 37  
 <211> 408  
 <212> DNA  
 <213> *Macaca cynomolgus*  
 <220>  
 <221> CDS  
 <222> (1)...(408)

<400> 37  
 atg gag ttt gga ctg agc tgg gtt ttc ctt gtc gct att ttc aaa ggt 48  
 Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Phe Lys Gly  
 1 5 10 15  
 gtc cag tgt gaa gtg cag ttg gtg gag tct ggg gga ggc ttg gta cag 96  
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
 20 25 30  
 ccg ggg ggg tcc ctg aga ctc gcc tgt gta ggc tct gga ttc gcc ttc 144  
 Pro Gly Gly Ser Leu Arg Leu Ala Cys Val Gly Ser Gly Phe Ala Phe  
 35 40 45  
 aga aac acc agg atg cac tgg att cga cag act cca gga aag agg ctg 192  
 Arg Asn Thr Arg Met His Trp Ile Arg Gln Thr Pro Gly Lys Arg Leu  
 50 55 60  
 gag tgg gtg gcc gac ata aag ttt gat gga agt gat ttt tac tat gta 240  
 Glu Trp Val Ala Asp Ile Lys Phe Asp Gly Ser Asp Phe Tyr Tyr Val  
 65 70 75 80  
 gac tct gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac 288  
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 85 90 95  
 tcc ctc tat ctg gaa atg aac agc ctg aga cct gat gac aca gcc gtc 336

Ser Leu Tyr Leu Glu Met Asn Ser Leu Arg Pro Asp Asp Thr Ala Val  
 100 105 110

tat ttc tgt gtg aga gaa tac aga gat gga ctg gat gtc tgg ggc cgg 384  
 Tyr Phe Cys Val Arg Glu Tyr Arg Asp Gly Leu Asp Val Trp Gly Arg  
 115 120 125

gga gtt ctg gtc acc gtc tcc tca 408  
 Gly Val Leu Val Thr Val Ser Ser  
 130 135

<210> 38  
 <211> 381  
 <212> DNA  
 <213> Macaca cynomolgus

<220>  
 <221> CDS  
 <222> (1)...(381)

<400> 38  
 gtg aca gct ccc aga tgg gtc ctg tcc cag gtg caa ttg cag gag tcg 48  
 Val Thr Ala Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Glu Ser  
 1 5 10 15

ggc cca gga ctg gtg aag cct tcg gag acc ctg tcc ctc act tgt act 96  
 Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr  
 20 25 30

gtc tct ggt gac tcc atc acc act gtc ttc tgg agc tgg ctc cgc cag 144  
 Val Ser Gly Asp Ser Ile Thr Thr Val Phe Trp Ser Trp Leu Arg Gln  
 35 40 45

tcg cca ggg att ggg ctg gag tgg att ggg aat ttt gct ggt agt act 192  
 Ser Pro Gly Ile Gly Leu Glu Trp Ile Gly Asn Phe Ala Gly Ser Thr  
 50 55 60



```

Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe
      35              40              45

acc gac agc tgg atc agc tgg gtg cgc cag atg ccc ggg aaa ggc ctg      192
Thr Asp Ser Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu
      50              55              60

gag tgg atg gga aac atc tat cct ggt gat tct gat tcc aga tac aac      240
Glu Trp Met Gly Asn Ile Tyr Pro Gly Asp Ser Asp Ser Arg Tyr Asn
      65              70              75              80

ccg tcc ttc caa ggc cgc gtc act atc tca gtc gac aag tcc atc agt      288
Pro Ser Phe Gln Gly Arg Val Thr Ile Ser Val Asp Lys Ser Ile Ser
      85              90              95

acc acc tac ctg cag tgg agc agc ctg aag gcc tgg gac act gcc aca      336
Thr Thr Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Thr
      100             105             110

tat tac tgt gcg aag ata gat agc aac tac tac agc cgg ttc gaa gtc      384
Tyr Tyr Cys Ala Lys Ile Asp Ser Asn Tyr Tyr Ser Arg Phe Glu Val
      115             120             125

tgg ggc ccc gga gtc atg gtc acc gtc tcc tca      417
Trp Gly Pro Gly Val Met Val Thr Val Ser Ser
      130             135

```

&lt;210&gt; 40

&lt;211&gt; 423

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(423)



&lt;400&gt; 40

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct cct aga tgg	48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
1 5 10 15	

gtc ctg tcc cag gtg cag ttg cag gag tgc ggc cca gga gtg gtg aag	96
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys	
20 25 30	

cct tgc gag acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc ttc	144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe	
35 40 45	

agt act tac tac tgg aat tgg atc cgc cag ccc cca ggg aag gga ctg	192
Ser Thr Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu	
50 55 60	

gag tgg att gga tat atc ggt ggt ggt ggt ggt cgc ccc aac tac aat	240
Glu Trp Ile Gly Tyr Ile Gly Gly Gly Gly Gly Arg Pro Asn Tyr Asn	
65 70 75 80	

tcc tcc ctc aag agt cgc atc acc ctg tca cta gac gcg tcc aag aac	288
Ser Ser Leu Lys Ser Arg Ile Thr Leu Ser Leu Asp Ala Ser Lys Asn	
85 90 95	

cag ttc tcc ctg aac ctg agc tct gtg acc gcc gcg gac acg gcc gtg	336
Gln Phe Ser Leu Asn Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	

tac tac tgt gcc aga gat cgg ggc tac ggt gcc agc aat gat gct ttt	384
Tyr Tyr Cys Ala Arg Asp Arg Gly Tyr Gly Ala Ser Asn Asp Ala Phe	
115 120 125	

gat ttc tgg ggc caa ggg ctc agg gtc acc gtc tct tca	423
Asp Phe Trp Gly Gln Gly Leu Arg Val Thr Val Ser Ser	
130 135 140	

<210> 41  
 <211> 411  
 <212> DNA  
 <213> *Macaca cynomolgus*

<220>  
 <221> CDS  
 <222> (1)...(411)

<400> 41

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca act cct aaa tgg	48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Thr Pro Lys Trp	
1 5 10 15	
gtc ctg tcc cag gtg cag ttg cat gag tgg ggc cct gga ctg ctg aag	96
Val Leu Ser Gln Val Gln Leu His Glu Ser Gly Pro Gly Leu Leu Lys	
20 25 30	
cct tgg gag acc ctg tcc ctc acc tgc aat gtc tcc ggt gac tcc ccc	144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Asn Val Ser Gly Asp Ser Pro	
35 40 45	
act aag tcc acg tgg aac tgg gtc cgc cag tcc cca ggg aag cca ctg	192
Thr Lys Ser Thr Trp Asn Trp Val Arg Gln Ser Pro Gly Lys Pro Leu	
50 55 60	
gaa tgg att ggt cat gtc ggt tct ggt gga ggt ggc ccc gtt tac aac	240
Glu Trp Ile Gly His Val Gly Ser Gly Gly Gly Gly Pro Val Tyr Asn	
65 70 75 80	
gtc ttc ttg acg ggt cgc gtc tcc atg tct cta gac gct tca aag aag	288
Val Phe Leu Thr Gly Arg Val Ser Met Ser Leu Asp Ala Ser Lys Lys	
85 90 95	
ctt ctc tcc ctg gcc tta gca tct gtg acc gcc gcc gac tgg gcc gtc	336
Leu Leu Ser Leu Ala Leu Ala Ser Val Thr Ala Ala Asp Ser Ala Val	

100

105

110

tat tac tgt gtc aga tcg acg gca tta ttt tcg ttg gat gtc tgg ggc 384  
 Tyr Tyr Cys Val Arg Ser Thr Ala Leu Phe Ser Leu Asp Val Trp Gly

115

120

125

cgg gga ctt ctg gtc acc gtc tcc tca 411  
 Arg Gly Leu Leu Val Thr Val Ser Ser

130

135

&lt;210&gt; 42

&lt;211&gt; 442

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(441)

&lt;400&gt; 42

atg gag ttg gga ctg agc tgg gtt ttc ctt ctt gtt gct att tta aaa 48  
 Met Glu Leu Gly Leu Ser Trp Val Phe Leu Leu Val Ala Ile Leu Lys  
 1 5 10 15

ggg gtc cag tgt gac aag cag ctg gtg cag tcg ggg gga ggc ttg gtc 96  
 Gly Val Gln Cys Asp Lys Gln Leu Val Gln Ser Gly Gly Gly Leu Val  
 20 25 30

cag cct ggc ggg tct ctg aga ctc gcc tgt gta gcc tcc gga ttc ccc 144  
 Gln Pro Gly Gly Ser Leu Arg Leu Ala Cys Val Ala Ser Gly Phe Pro  
 35 40 45

ttc agt gac tat tac atg agt tgg gtc cgc cag gct cca ggg aag ggg 192  
 Phe Ser Asp Tyr Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly  
 50 55 60

ttc cgc ttc a 442  
Phe Arg Phe  
145

<210> 43  
<211> 407  
<212> DNA  
<213> *Macaca cynomolgus*

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<220>  
<221> CDS  
<222> (1) ... (405)
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<400> 43  
atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg 48  
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

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<210> 44
<211> 420
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&lt;212&gt; DNA

<213> *Macaca cynomolgus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(420)

&lt;400&gt; 44

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg 48

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

1 5 10 15

gtc ctg tcc cag gtt caa cta cag gag tgg ggc cca gga ctg atg aag 96

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Met Lys

20 25 30

cct tgg gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tcc atc 144

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile

35 40 45

agc ggt ggt ttt ggc tgg ggc tgg atc cgt cag tcc ccg ggg aag ggg 192

Ser Gly Gly Phe Gly Trp Gly Trp Ile Arg Gln Ser Pro Gly Lys Gly

50 55 60

ctg gaa tgg att gga agt ttc tat act act act gga aat acc ttc tcc 240

Leu Glu Trp Ile Gly Ser Phe Tyr Thr Thr Thr Gly Asn Thr Phe Ser

65 70 75 80

aac ccc tcc ctc aag agt cga gtc acc att tca gcg gac acg tcc aag 288

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ala Asp Thr Ser Lys

85 90 95

aac cag ttc tcc ctg aga ctg acc tct gtg acc gcc gcg gac acg gcc 336

Asn Gln Phe Ser Leu Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala

100 105 110

gtt tat tac tgt gcg aga gat ctc tat agc agc ggc tat aaa ttt tac 384

Val Tyr Tyr Cys Ala Arg Asp Leu Tyr Ser Ser Gly Tyr Lys Phe Tyr  
 115 120 125

tac tgg ggc cag gga gtc ctg gtc acc gtc tcc tca 420  
 Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
 130 135 140

<210> 45  
 <211> 98  
 <212> PRT  
 <213> *Macaca cynomolgus*

<220>  
 <221> DOMAIN  
 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 45

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ala Cys Val Gly Ser Gly Phe Ala Phe Arg Asn Thr  
 20 25 30  
 Arg Met His Trp Ile Arg Gln Thr Pro Gly Lys Arg Leu Glu Trp Val  
 35 40 45  
 Ala Asp Ile Lys Phe Asp Gly Ser Asp Phe Tyr Tyr Val Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80  
 Leu Glu Met Asn Ser Leu Arg Pro Asp Asp Thr Ala Val Tyr Phe Cys  
 85 90 95  
 Val Arg

<210> 46  
 <211> 98  
 <212> PRT  
 <213> *Macaca cynomolgus*

<220>  
 <221> DOMAIN  
 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 46  
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Thr Thr Val  
 20 25 30  
 Phe Trp Ser Trp Leu Arg Gln Ser Pro Gly Ile Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Asn Phe Ala Gly Ser Thr Pro Glu Thr Asn Tyr Asn Pro Ser Leu  
 50 55 60  
 Lys Asn Arg Ala Thr Ile Ser Lys Asp Thr Pro Thr Asn Gln Phe Phe  
 65 70 75 80  
 Leu Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys  
 85 90 95  
 Ala Arg

<210> 47  
 <211> 98  
 <212> PRT  
 <213> *Macaca cynomolgus*

<220>



&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 47

Glu Val His Leu Val Gln Ser Gly Ala Gln Val Lys Arg Pro Gly Glu  
 1 5 10 15  
 Ser Leu Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Asp Ser  
 20 25 30  
 Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45  
 Gly Asn Ile Tyr Pro Gly Asp Ser Asp Ser Arg Tyr Asn Pro Ser Phe  
 50 55 60  
 Gln Gly Arg Val Thr Ile Ser Val Asp Lys Ser Ile Ser Thr Thr Tyr  
 65 70 75 80  
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Thr Tyr Tyr Cys  
 85 90 95  
 Ala Lys

&lt;210&gt; 48

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 48

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys Pro Ser Glu  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr  
 20 25 30  
 Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Tyr Ile Gly Gly Gly Gly Gly Arg Pro Asn Tyr Asn Ser Ser Leu  
 50 55 60  
 Lys Ser Arg Ile Thr Leu Ser Leu Asp Ala Ser Lys Asn Gln Phe Ser  
 65 70 75 80  
 Leu Asn Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg

&lt;210&gt; 49

&lt;211&gt; 98

&lt;212&gt; PRT

<213> *Macaca cynomolgus*

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31) ... (35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50) ... (66)

&lt;223&gt; CDRII

&lt;400&gt; 49

Gln Val Gln Leu His Glu Ser Gly Pro Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Asn Val Ser Gly Asp Ser Pro Thr Lys Ser  
 20 25 30  
 Thr Trp Asn Trp Val Arg Gln Ser Pro Gly Lys Pro Leu Glu Trp Ile

```

          35              40              45
Gly His Val Gly Ser Gly Gly Gly Gly Pro Val Tyr Asn Val Phe Leu
  50              55              60
Thr Gly Arg Val Ser Met Ser Leu Asp Ala Ser Lys Lys Leu Leu Ser
  65              70              75              80
Leu Ala Leu Ala Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys
          85              90              95
Val Arg

```

```

<210> 50
<211> 100
<212> PRT
<213> Macaca cynomolgus

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<220>
<221> DOMAIN
<222> (31)...(35)
<223> CDRI

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<221> DOMAIN
<222> (50)...(68)
<223> CDRII

```

```

<400> 50
Asp Lys Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
  1              5              10              15
Ser Leu Arg Leu Ala Cys Val Ala Ser Gly Phe Pro Phe Ser Asp Tyr
  20              25              30
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
  35              40              45
Gly Leu Ile Lys Thr Asn Pro Asp Gly Gly Thr Thr Asp Tyr Ala Ala
  50              55              60
Ser Val Lys Gly Arg Phe Ile Ile Ser Arg Asp Asp Ser Lys Asn Ser
  65              70              75              80
Leu Phe Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
          85              90              95

```

Tyr Cys Thr Thr

100

&lt;210&gt; 51

&lt;211&gt; 98

&lt;212&gt; PRT

<213> *Macaca cynomolgus*

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 51

Gln Val Gln Leu Glu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Leu Ile Thr Gly Asn

20 25 30

Tyr Trp Asn Trp Leu Arg Gln Ser Glu Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly His Ile Gly Gly Ser Ser Gly Asn Thr Gly Tyr Asn Ser Ala Phe

50 55 60

Glu Ser Arg Val Thr Leu Ser Arg Asp Thr Ala Lys Asn Arg Phe Ser

65 70 75 80

Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys

85 90 95

Ala Arg

&lt;210&gt; 52

&lt;211&gt; 99

&lt;212&gt; PRT

<213> *Macaca cynomolgus*

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(36)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (51)...(67)

&lt;223&gt; CDRII

&lt;400&gt; 52

```

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Met Lys Pro Ser Glu
 1             5             10             15
Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Gly Gly
      20             25             30
Phe Gly Trp Gly Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp
      35             40             45
Ile Gly Ser Phe Tyr Thr Thr Thr Gly Asn Thr Phe Ser Asn Pro Ser
      50             55             60
Leu Lys Ser Arg Val Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe
      65             70             75             80
Ser Leu Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
      85             90             95
Cys Ala Arg

```

&lt;210&gt; 53

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(390)

&lt;400&gt; 53

```

atg gac ata agg gtc ccc gtg cag ctc ctg ggg ctc ctg ttg ctc tgg

```

48

Met Asp Ile Arg Val Pro Val Gln Leu Leu Gly Leu Leu Leu Leu Trp	
1 5 10 15	
ctc cga ggt gcc aga tgt gac atc cag atg acc cag tct cca tcc tcc	96
Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
20 25 30	
ctg tct aca tct gta gga gac act gtc acc atc act tgc cgg gcg agt	144
Leu Ser Thr Ser Val Gly Asp Thr Val Thr Ile Thr Cys Arg Ala Ser	
35 40 45	
caa ggc att gac acg gag tta gcc tgg tat cag cag aaa cca ggt aaa	192
Gln Gly Ile Asp Thr Glu Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys	
50 55 60	
gcc ccc aca ctc ctg atc tct gat gcc tcc agg ttg cag acg ggg gtc	240
Ala Pro Thr Leu Leu Ile Ser Asp Ala Ser Arg Leu Gln Thr Gly Val	
65 70 75 80	
tca tct cgg ttc agc ggc agt gga tct gga aca gat ttc act ctc acc	288
Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
85 90 95	
atc aac agc ctg cag cct gaa gat att gcg act tat tac tgt caa cag	336
Ile Asn Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln	
100 105 110	
gat aat agt ttt cca ctc act ttc ggc gga ggg acc aag gtg gag atc	384
Asp Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile	
115 120 125	
aaa cga	390
Lys Arg	
130	

&lt;210&gt; 54

&lt;211&gt; 384

&lt;212&gt; DNA

<213> *Macaca cynomolgus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(384)

&lt;400&gt; 54

gtc ttc att tcc ctg ttg ctc tgg atc tct ggt gcc tgt ggg gac att	48
Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Cys Gly Asp Ile	
1 5 10 15	

gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg gga gag agg	96
Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg	
20 25 30	

gtc acc atc aat tgt aag tcc agc cag agt ctt tta tac agc tcc aac	144
Val Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn	
35 40 45	

aat aag aac tac tta gcc tgg tac cag caa aaa cca gga cag gct cct	192
Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro	
50 55 60	

caa cta ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc cct aat	240
Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asn	
65 70 75 80	

cga ttt agt ggc agc ggc tct ggg aca gat ttc act ctc acc atc agt	288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser	
85 90 95	

ggc ctg cag gct gaa gat gtg gca gtg tat tac tgt caa cag tat tat	336
Gly Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr	
100 105 110	

gat atg ccc gac agt ttt ggc cag ggg acc aaa gtg gac atc aaa cga 384  
 Asp Met Pro Asp Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg  
 115 120 125

<210> 55  
 <211> 399  
 <212> DNA  
 <213> *Macaca cynomolgus*

<220>  
 <221> CDS  
 <222> (1)...(399)

<400> 55  
 atg agg ctc cct gct cag ctc ctg ggg ctg cta ttg ctc tgc gtc ccc 48  
 Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys Val Pro  
 1 5 10 15

gga tcc agt ggg gat gtt gtg atg act cag tct cca ctc tcc ctg ccc 96  
 Gly Ser Ser Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro  
 20 25 30

gtc atc cct gga cag cca gcc tcc atc tcc tgc agg tct agt caa agc 144  
 Val Ile Pro Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser  
 35 40 45

ctt gta cat agt gac ggg aaa acc tac ttg aat tgg tta caa cag aag 192  
 Leu Val His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Lys  
 50 55 60

cca ggc caa cct cca aga ctc ctg att tat cag gtt tct aac cgg cac 240  
 Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Gln Val Ser Asn Arg His  
 65 70 75 80

tct ggg gtc cca gac aga ttc agc ggc agt ggg gca ggg aca gac ttc 288  
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe



85

90

95

aca ctg aaa atc agc aga gtg gag act gag gat gtt ggg gtt tat tcc 336  
 Thr Leu Lys Ile Ser Arg Val Glu Thr Glu Asp Val Gly Val Tyr Ser

100

105

110

tgc gtg caa ggt aca cac tgg ccg tgg acg ttc ggc caa ggg acc aag 384  
 Cys Val Gln Gly Thr His Trp Pro Trp Thr Phe Gly Gln Gly Thr Lys

115

120

125

gtg gac atc aaa cga 399  
 Val Asp Ile Lys Arg

130

&lt;210&gt; 56

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(384)

&lt;400&gt; 56

atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc cca 48  
 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro  
 1 5 10 15

ggt gcc ata tgt gac att cag atg tcc cag tct cca tcc tcc ctg tct 96  
 Gly Ala Ile Cys Asp Ile Gln Met Ser Gln Ser Pro Ser Ser Leu Ser  
 20 25 30

gct tct gtg gga gac aga gtc acc atc acc tgc cgg gca agt cag ggc 144  
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly  
 35 40 45

ata act aat tat tta aac tgg tat cag cag aaa ccg ggg aaa gcc cct 192  
 Ile Thr Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
 50 55 60

aac ctc ctg atc tat tat gca act cgt ttg gcg agc ggg gtc cca tca 240  
 Asn Leu Leu Ile Tyr Tyr Ala Thr Arg Leu Ala Ser Gly Val Pro Ser  
 65 70 75 80

agg ttc agc ggc agt gga tct ggg tcg gag tac agt ctc gcc atc agc 288  
 Arg Phe Ser Gly Ser Gly Ser Gly Ser Glu Tyr Ser Leu Ala Ile Ser  
 85 90 95

agc ctg cag cct gaa gat ttt gca acc tat ttc tgt caa cag ggt tat 336  
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Tyr  
 100 105 110

agg gcc ccc tac act ttt ggc cag ggg acc aca gtg gag atc aaa cga 384  
 Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg  
 115 120 125

<210> 57

<211> 390

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1)...(390)

<400> 57

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48  
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

ctc cta ggt gcc aga tgt gac atc cag atg acc cag tct cct tct tcc 96  
 Leu Leu Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser

20

25

30

ttg tct gca tct gta gga gac aga gtc acc atc act tgc caa gcc agt 144  
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser

35

40

45

cag ggt att agc aac tgg tta gcc tgg tat cag cag aaa ccg ggg aaa 192  
 Gln Gly Ile Ser Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys

50

55

60

gcc cct aag ctc ctg atc tat gct gca tcc act ttc caa agt ggg gtc 240  
 Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Phe Gln Ser Gly Val

65

70

75

80

cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc 288  
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr

85

90

95

atc agc agc ctg cag cct gaa gat ttt gca act tac tac tgt caa cag 336  
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln

100

105

110

tat aat act tac cct ctc act ttc ggc gga ggg acc aag gtg gag atc 384  
 Tyr Asn Thr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile

115

120

125

aaa cga 390  
 Lys Arg

130

&lt;210&gt; 58

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(390)

&lt;400&gt; 58

atg gac ttg agg gcc ccc gct cat ctc cta ggg ctc ctg ctg ctc tgg	48
Met Asp Leu Arg Ala Pro Ala His Leu Leu Gly Leu Leu Leu Leu Trp	
1 5 10 15	
ctc cca ggt gcc aga ggt gac atc cag atg acc cag tct cca ccc tcc	96
Leu Pro Gly Ala Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Pro Ser	
20 25 30	
ctg tct gcg tct gtt ggg gac act gtc agt ctt act tgt cgg gca agt	144
Leu Ser Ala Ser Val Gly Asp Thr Val Ser Leu Thr Cys Arg Ala Ser	
35 40 45	
cag cct att ggc agt aat tta aat tgg ttc cag caa aaa cct ggg agc	192
Gln Pro Ile Gly Ser Asn Leu Asn Trp Phe Gln Gln Lys Pro Gly Ser	
50 55 60	
ccc ccc aga ctc ctg atc tac ctt gcg acc gcc ttg caa cgt ggg atc	240
Pro Pro Arg Leu Leu Ile Tyr Leu Ala Thr Ala Leu Gln Arg Gly Ile	
65 70 75 80	
ccg tca agg ttt agc gcc act gga tct caa acc aat ttc act ctc acg	288
Pro Ser Arg Phe Ser Ala Thr Gly Ser Gln Thr Asn Phe Thr Leu Thr	
85 90 95	
atc acc ggc ctg cag cct gag gat ttc gca act tac ctc tgt ctg caa	336
Ile Thr Gly Leu Gln Pro Glu Asp Phe Ala Thr Tyr Leu Cys Leu Gln	
100 105 110	
cat act tct tac cca ttc act ttt ggc ccc ggg aca aag gtg gat atc	384
His Thr Ser Tyr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile	
115 120 125	
aag cga	390

Lys Arg

130

&lt;210&gt; 59

&lt;211&gt; 88

&lt;212&gt; PRT

<213> *Macaca cynomolgus*

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(56)

&lt;223&gt; CDRII

&lt;400&gt; 59

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Thr	Ser	Val	Gly
1				5					10					15	
Asp	Thr	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Asp	Thr	Glu
			20				25						30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Thr	Leu	Leu	Ile
		35				40						45			
Ser	Asp	Ala	Ser	Arg	Leu	Gln	Thr	Gly	Val	Ser	Ser	Arg	Phe	Ser	Gly
	50					55				60					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Ser	Leu	Gln	Pro
65				70					75					80	
Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys								
				85											

&lt;210&gt; 60

&lt;211&gt; 94

&lt;212&gt; PRT

<213> *Macaca cynomolgus*

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(40)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (56)...(62)

&lt;223&gt; CDRII

&lt;400&gt; 60

```

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1             5             10             15
Glu Arg Val Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
      20             25             30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
      35             40             45
Ala Pro Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
      50             55             60
Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
      65             70             75             80
Ile Ser Gly Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
      85             90

```

&lt;210&gt; 61

&lt;211&gt; 93

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(39)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (54)...(61)

&lt;223&gt; CDRII

&lt;400&gt; 61

Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Ile	Pro	Gly
1				5					10					15	
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser
		20						25					30		
Asp	Gly	Lys	Thr	Tyr	Leu	Asn	Trp	Leu	Gln	Gln	Lys	Pro	Gly	Gln	Pro
		35					40					45			
Pro	Arg	Leu	Leu	Ile	Tyr	Gln	Val	Ser	Asn	Arg	His	Ser	Gly	Val	Pro
	50					55				60					
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ala	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65					70					75				80	
Ser	Arg	Val	Glu	Thr	Glu	Asp	Val	Gly	Val	Tyr	Ser	Cys			
				85				90							

&lt;210&gt; 62

<211> 88

<212> PRT

<213> *Macaca cynomolgus*

 $\langle 220 \rangle$ 

&lt;221&gt; DOMAIN

 $\langle 222 \rangle \quad (24) \dots (34)$ 

&lt;223&gt; CDR1

&lt;221&gt; DOMAIN

<222> (50) . . . (56)

&lt;223&gt; CDRII

<400> 62

Asp	Ile	Gln	Met	Ser	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Thr	Asn	Tyr
				20				25					30		
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Asn	Leu	Leu	Ile
				35			40					45			
Tyr	Tyr	Ala	Thr	Arg	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

```
<210> 63
<211> 88
<212> PRT
<213> Macaca cynomolgus
```

```
<220>  
<221> DOMAIN  
<222> (24) ... (34)  
<223> CDR1
```

```
<221> DOMAIN
<222> (50) ... (56)
<223> CDRII
```

```

<400> 63
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1          5          10          15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Gly Ile Ser Asn Trp
          20          25          30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35          40          45
Tyr Ala Ala Ser Thr Phe Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65          70          75          80
Glu Asp Phe Ala Thr Tyr Tyr Cys
          85

```

```
<210> 64
<211> 88
<212> PRT
<213> Macaca cynomolgus
```



&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(56)

&lt;223&gt; CDRII

&lt;400&gt; 64

```

Asp Ile Gln Met Thr Gln Ser Pro Pro Ser Leu Ser Ala Ser Val Gly
 1             5             10             15
Asp Thr Val Ser Leu Thr Cys Arg Ala Ser Gln Pro Ile Gly Ser Asn
      20             25             30
Leu Asn Trp Phe Gln Gln Lys Pro Gly Ser Pro Pro Arg Leu Leu Ile
      35             40             45
Tyr Leu Ala Thr Ala Leu Gln Arg Gly Ile Pro Ser Arg Phe Ser Ala
      50             55             60
Thr Gly Ser Gln Thr Asn Phe Thr Leu Thr Ile Thr Gly Leu Gln Pro
      65             70             75             80
Glu Asp Phe Ala Thr Tyr Leu Cys
      85

```

&lt;210&gt; 65

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(360)

&lt;400&gt; 65

```

gac acg gtg ctg acc cag tct cct gct ttg gct gtg cct cca gga gag
Asp Thr Val Leu Thr Gln Ser Pro Ala Leu Ala Val Pro Gly Glu
 1             5             10             15

```

48

agg gtt acc gtc tcc tgt agg gcc agt gaa agt gtc agt aca ttt ttg	96
Arg Val Thr Val Ser Cys Arg Ala Ser Glu Ser Val Ser Thr Phe Leu	
20 25 30	
cac tgg tat caa cag aaa cca gga cat caa ccc aaa ctc ctc atc tat	144
His Trp Tyr Gln Gln Lys Pro Gly His Gln Pro Lys Leu Leu Ile Tyr	
35 40 45	
cta gcc tca aaa cta gaa tct ggg gtc cct gcc agg ttc agt ggc ggt	192
Leu Ala Ser Lys Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Gly	
50 55 60	
ggg tct ggg aca gac ttc acc ctc acc att gat cct gtg gag gct gat	240
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asp Pro Val Glu Ala Asp	
65 70 75 80	
gac act gct acc tat tac tgt cag cag acc tgg aat gat cct cgg acg	288
Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Thr Trp Asn Asp Pro Arg Thr	
85 90 95	
ttc ggt gga ggc acc aag ctg gaa ttg aaa cgg gct gat gct gca cca	336
Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro	
100 105 110	
act gta tct atc ttc cca cca tcc	360
Thr Val Ser Ile Phe Pro Pro Ser	
115 120	

&lt;210&gt; 66

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(360)

&lt;400&gt; 66

gag gtc cag ctg cag cag tct gga cct gag gtt ggg agg cct ggg tcc	48
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Val Gly Arg Pro Gly Ser	
1 5 10 15	
tca gtc aag att tct tgc aag gct tct ggc tac acc ttt aca gat tac	96
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr	
20 25 30	
gtt ttg aat tgg gtg aag cag agt cct gga cag gga ctg gaa tgg ata	144
Val Leu Asn Trp Val Lys Gln Ser Pro Gly Gln Gly Leu Glu Trp Ile	
35 40 45	
gga tgg att gat cct gac tat ggt act act gat tat gct gag aag ttc	192
Gly Trp Ile Asp Pro Asp Tyr Gly Thr Thr Asp Tyr Ala Glu Lys Phe	
50 55 60	
aaa aag aag gcc aca ctg act gca gat aca tcc tcc agc aca gcc tac	240
Lys Lys Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Thr Ala Tyr	
65 70 75 80	
atc cag ctt agc agc ctg aca tct gag gac aca gcc acc tat ttt tgt	288
Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Thr Tyr Phe Cys	
85 90 95	
gct aga tct agg aat tac gga gga tat att aat tac tgg ggc caa gga	336
Ala Arg Ser Arg Asn Tyr Gly Gly Tyr Ile Asn Tyr Trp Gly Gln Gly	
100 105 110	
gtc atg gtc aca gtc tcc tca gct	360
Val Met Val Thr Val Ser Ser Ala	
115 120	

&lt;210&gt; 67

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 67

Ala	Val	His	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5						10				15	
Asp	Ser	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Thr	Ile	Asn	Ile	Tyr
				20				25						30	
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
				35				40						45	
Phe	Asp	Ala	Ser	Ile	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
				50				55						60	
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Ser	Leu	Thr	Ile	Arg	Ser	Leu	Gln	Pro
65					70					75				80	
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Cys	Gly	Trp	Gly	Thr	His	Pro
					85					90				95	
Tyr	Asn	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg			
				100						105					

&lt;210&gt; 68

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; rat/chimpanzee sequence

&lt;400&gt; 68

Asp	Thr	Val	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1					5					10				15	
Asp	Ser	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Glu	Ser	Val	Ser	Thr	Phe
				20				25						30	
Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
				35				40						45	
Tyr	Leu	Ala	Ser	Lys	Leu	Glu	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly
				50				55						60	

Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Arg Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Trp Asn Asp Pro Arg  
 85 90 95  
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
 100 105

<210> 69  
 <211> 128  
 <212> PRT  
 <213> Pan troglodytes

<400> 69  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Phe  
 20 25 30  
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45  
 Ser Leu Val Ser Trp Asp Ser Tyr Asn Ile Tyr His Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Ser Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Asp Leu Arg Pro Glu Asp Thr Ala Ile Tyr Phe Cys  
 85 90 95  
 Ala Lys Ala Asp Thr Gly Gly Asp Phe Asp Tyr Val Ser Asp Ser Trp  
 100 105 110  
 Arg Cys Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
 115 120 125

<210> 70  
 <211> 118  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> rat/chimpanzee sequence

&lt;400&gt; 70

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asp Tyr  
 20 25 30  
 Val Leu Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Trp Ile Asp Pro Asp Tyr Gly Thr Thr Asp Tyr Ala Glu Lys Phe  
 50 55 60  
 Lys Lys Lys Ala Thr Leu Ser Ala Asp Thr Ser Arg Asn Ser Ala Tyr  
 65 70 75 80  
 Leu Gln Met Asn Asp Leu Arg Pro Glu Asp Thr Ala Ile Tyr Phe Cys  
 85 90 95  
 Ala Arg Ser Arg Asn Tyr Gly Gly Tyr Ile Asn Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser  
 115

&lt;210&gt; 71

&lt;211&gt; 354

&lt;212&gt; DNA

&lt;213&gt; Murine

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(354)

&lt;400&gt; 71

caa gtt cag ctt caa cag tct gga gct gag ctg atg aag cct ggg gcc 48  
 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala  
 1 5 10 15  
 tca gtg aag ata tcc tgc aag gct act ggc tac aca ttc agt agc tac 96  
 Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr  
 20 25 30

tgg ata gag tgg gta aag cag agg cct gga cat ggc ctt gag tgg att 144  
 Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile  
 35 40 45

gga gag att tta cct aga agt ggt aat act aac tac aat gag aag ttc 192  
 Gly Glu Ile Leu Pro Arg Ser Gly Asn Thr Asn Tyr Asn Glu Lys Phe  
 50 55 60

aag ggc aag gcc aca ttc act gca gaa aca tcc tcc aac aca gcc tac 240  
 Lys Gly Lys Ala Thr Phe Thr Ala Glu Thr Ser Ser Asn Thr Ala Tyr  
 65 70 75 80

atg caa ctc agc agc ctg aca cct gag gac tct gcc gtc tat tac tgt 288  
 Met Gln Leu Ser Ser Leu Thr Pro Glu Asp Ser Ala Val Tyr Tyr Cys  
 85 90 95

tca agt cgc ggc gtc agg ggc tct atg gac tac tgg ggt caa gga acc 336  
 Ser Ser Arg Gly Val Arg Gly Ser Met Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110

tca gtc acc gtc tcc tca 354  
 Ser Val Thr Val Ser Ser  
 115

. <210> 72  
 <211> 324  
 <212> DNA  
 <213> Murine

<220>  
 <221> CDS  
 <222> (1)...(324)

<400> 72  
 gat att cag atg acc cag act aca tcc tcc ctg tct gcc tct ctg gga 48  
 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly

1	5	10	15	
gac aga gtc acc atc act tgc agg tca agt cag gac att agc aat ttt				96
Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Asp Ile Ser Asn Phe				
20		25	30	
tta aac tgg tat cag cag aaa cca gat gga act gtt aaa ctc ctg atc				144
Leu Asn Trp Tyr Thr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile				
35	40		45	
tac tac aca tca aca tta cac tca gga gtc cca tca agg ttc agt ggc				192
Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly				
50	55	60		
agt ggg tct gga aca gat tat tct ctc acc att agc aac ctg gag caa				240
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln				
65	70	75	80	
gaa gat att gcc act tac ttt tgc caa cag ggt aat acg ctt cct tgg				288
Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp				
85	90	95		
acg ttc ggt gga ggc acc aac ctg gaa atc aaa cgg				324
Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys Arg				
100	105			

&lt;210&gt; 73

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; murine/chimpanzee sequence

&lt;400&gt; 73

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly



1					5					10					15				
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ser	Ser	Gln	Asp	Ile	Ser	Asn	Phe				
				20				25				30							
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile				
				35				40				45							
Tyr	Tyr	Thr	Ser	Thr	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly				
				50				55				60							
Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro				
65				70				75				80							
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Trp				
				85				90				95							
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg								
				100				105											

<210> 74

&lt;211&gt; 118

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> murine/chimpanzee sequence

&lt;400&gt; 74

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Ser	Ser	Tyr
			20						25					30	
Trp	Ile	Glu	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
			35				40						45		
Gly	Glu	Ile	Leu	Pro	Arg	Ser	Gly	Asn	Thr	Asn	Tyr	Asn	Glu	Lys	Phe
			50				55				60				
Lys	Gly	Lys	Ala	Ser	Phe	Asn	Ala	Asp	Thr	Ser	Thr	Asn	Ile	Ala	Tyr
65					70					75				80	
Met	Glu	Leu	Thr	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ser	Ser	Arg	Gly	Val	Arg	Gly	Ser	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
				100					105					110	

Leu Val Thr Val Ser Ser

115

&lt;210&gt; 75

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Murine

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(360)

&lt;400&gt; 75

caa gtt cag ctt caa cag cct ggg gct gag ctt gtg aag tct ggg gcc	48
-----------------------------------------------------------------	----

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Ser Gly Ala	
-----------------------------------------------------------------	--

1	5	10	15
---	---	----	----

tca gtg aag ctg tcc tgc aag gct tct ggc agt acc ttc acc agc tac	96
-----------------------------------------------------------------	----

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Ser Thr Phe Thr Ser Tyr	
-----------------------------------------------------------------	--

20	25	30
----	----	----

tgg atg cac tgg gtg aag cag agg cct gga cga ggc ctt gag tgg att	144
-----------------------------------------------------------------	-----

Trp Met His Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile	
-----------------------------------------------------------------	--

35	40	45
----	----	----

gga agg att gat cca aat agt ggt ggt act aag gat aat gag aag ttc	192
-----------------------------------------------------------------	-----

Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Asp Asn Glu Lys Phe	
-----------------------------------------------------------------	--

50	55	60
----	----	----

aag agc aag gcc aca ctg act gta gac aaa ccc tcc agc aca gcc tac	240
-----------------------------------------------------------------	-----

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Pro Ser Ser Thr Ala Tyr	
-----------------------------------------------------------------	--

65	70	75	80
----	----	----	----

atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc tat tat tgt	288
-----------------------------------------------------------------	-----

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys	
-----------------------------------------------------------------	--

85	90	95
----	----	----

101

65 70 75 80

gaa gac ttg gca gag tat ttc tgt cag caa tat aac agc tat cct ctc 288

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu

85 90 95

acg ttc ggt gct ggg acc aag ctg gag ctg aaa cgg gct gat gct gca 336

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala

100 105 110

<210> 77

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> murine/chimpanzee sequence

<400> 77

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn

20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile

35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu

85 90 95

Thr Phe Gly Gly Thr Lys Val Glu Ile Lys

100 105

<210> 78

<211> 118

<213> Artificial Sequence

<223> murine/chimpanzee sequence

[illegible]

&lt;211&gt; 119

&lt;212&gt; PRT

<213> Art

<223> murine/human sequence

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Ser Thr Phe Thr Ser Tyr  
20 25 30

```

Trp Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
   35                               40                               45
Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Asp Asn Glu Lys Phe
   50                               55                               60
Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
   65                               70                               75                               80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
   85                               90                               95
Ala Arg Glu Thr Tyr Tyr Asp Ser Ser Phe Ala Tyr Trp Gly Gln Gly
  100                               105                               110
Thr Met Val Thr Val Ser Ala
  115

```

<210> 80

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> murine/human sequence

<400> 80

```

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
   1                               5                               10                               15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
  20                               25                               30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
  35                               40                               45
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Ser Gly
  50                               55                               60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
  65                               70                               75                               80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
  85                               90                               95
Thr Phe Gly Gly Gly Thr
  100

```

<400> 81  
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser  
1 5 10

<400> 82  
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
1 5 10

<400> 83  
Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser  
1 5 10

<400> 84  
Trp Gly Gln Gly Ile Leu Val Thr Val Ser Ser  
1 5 10

105

```
<211> 11
<212> PRT
<213> Pan troglodytes
```

<400> 85  
Trp Gly Arg Gly Ile Leu Val Ile Val Ser Ser  
1 5 10

```
<210> 86
<211> 11
<212> PRT
<213> Pan troglodytes
```

<400> 86  
Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg  
1 5 10

```
<210> 87
<211> 11
<212> PRT
<213> Pan troglodytes
```

<400> 87

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg

1 5 10

```
<210> 88
<211> 11
<212> PRT
<213> Macaca cynomolgus
```

<400> 88  
Trp Gly Arg Gly Val Leu Val Thr Val Ser Ser  
1 5 10

<210>	89
<211>	11



&lt;212&gt; PRT

<213> *Macaca cynomolgus*

&lt;400&gt; 89

Trp Gly Gln Gly Val Gln Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 90

&lt;211&gt; 11

&lt;212&gt; PRT

<213> *Macaca cynomolgus*

&lt;400&gt; 90

Trp Gly Pro Gly Val Met Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 91

&lt;211&gt; 11

&lt;212&gt; PRT

<213> *Macaca cynomolgus*

&lt;400&gt; 91

Trp Gly Arg Gly Leu Leu Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 92

&lt;211&gt; 11

&lt;212&gt; PRT

<213> *Macaca cynomolgus*

&lt;400&gt; 92

Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 93

&lt;211&gt; 11

&lt;212&gt; PRT

<213> Macaca cynomolgus

<400> 93

Trp Gly Gln Gly Leu Arg Val Thr Val Ser Ser

1 5 10

<210> 94

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 94

Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg

1 5 10

<210> 95

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 95

Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg

1 5 10

<210> 96

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 96

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg

1 5 10

<210> 97

<211> 11

<212> PRT

<213> Pan troglodytes

<400> 97

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg

1

5

10

109170.2425060